



09/674035

SEQUENCE LISTING

<110> Lang, Jas

<120> Detecting the Expression of the DESC1 Gene in Squamous Cell Carcinoma

<130> 22727/04078

<140> 09/674,035

<141> 1999-11-11

<150> PCT/IB99/01818

<151> 1999-11-11

<160> 10

<170> PatentIn version 3.0

<210> 1

<211> 1269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1269)

<400> 1

atg tat cgg cca gat gtg gtg agg gct agg aaa aga gtt tgt tgg gaa

48

Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu

1

5

10

15

ccc tgg gtt atc ggc ctc gtc atc ttc ata tcc ctg att gtc ctg gca

96

Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala

20

25

30

gtg tgc att gga ctc act gtt cat tat gtg aga tat aat caa aag aag

144

Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys

35

40

45

acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat
192

Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr

50

55

60

gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag
240

Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln

65

70

75

80

aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg
288

Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg

85

90

95

gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa gac aag cat
336

Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Asp Lys His

100

105

110

gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag
384

Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu

115

120

125

gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag
432

Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys

130

135

140

ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa
480

Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys

145 150 155 160

att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc
528

Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys

165 170 175

tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt
576

Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val

180 185 190

ggg gga aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg
624

Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu

195 200 205

cag tgg gat ggg agt cat gcg tgt gga gca acc tta att aat gcc aca
672

Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr

210 215 220

tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc
720

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala

225 230 235 240

aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa
768

Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys

245 250 255

cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca
816

Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser

260

265

270

cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac
864

His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr

275

280

285

aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt
912

Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe

290

295

300

caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat
960

Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn

305

310

315

320

gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata
1008

Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile

325

330

335

gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act
1056

Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr

340

345

350

cct aga atc tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc
1104

Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys

355

360

365

cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc
1152

Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile

370

375

380

tgg tac ctt gct gga ata gtg agc tgg gga gat gaa tgt gcg aaa ccc

1200

Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro

385

390

395

400

aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att

1248

Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile

405

410

415

act tca aaa act ggt atc taa

1269

Thr Ser Lys Thr Gly Ile

420

<210> 2

<211> 422

<212> PRT

<213> Homo sapiens

<400> 2

Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu

1

5

10

15

Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala

20

25

30

Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys

35

40

45

Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr

50

55

60

Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
65 70 75 80

Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
85 90 95

Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Asp Lys His
100 105 110

Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
115 120 125

Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
130 135 140

Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
145 150 155 160

Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
165 170 175

Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
180 185 190

Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
195 200 205

Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
210 215 220

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
225 230 235 240

Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
245 250 255

Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
260 265 270

His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
275 280 285

Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
290 295 300

Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
305 310 315 320

Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
325 330 335

Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
340 345 350

Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
355 360 365

Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
370 375 380

Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
385 390 395 400

Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
405 410 415

Thr Ser Lys Thr Gly Ile
420

<210> 3
<211> 1269

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1269)

<400> 3
atg tat cgg cca gat gtg gtg agg gct agg aaa aga gtt tgt tgg gaa
48
Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
1 5 10 15

ccc tgg gtt atc ggc ctc gtc atg ttc ata tcc ctg att gtc ctg gca
96
Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala
20 25 30

gtg tgc att gga gtc act gtt cat tat gtg aga tat aat caa aag aag
144
Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
35 40 45

acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat
192
Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
50 55 60

gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag
240
Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
65 70 75 80

aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg
288
Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
85 90 95

gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat
336

Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His

100

105

110

gga gtg ttg gct cat atg ctg ttg att tct aga ttt cac tct act gag
384

Gly Val Leu Ala His Met Leu Leu Ile Ser Arg Phe His Ser Thr Glu

115

120

125

gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag
432

Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys

130

135

140

ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa
480

Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys

145

150

155

160

att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc
528

Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys

165

170

175

tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt
576

Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val

180

185

190

ggg gga aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg
624

Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu

195	200	205
cag tgg gat ggg agt cat cgc tgt gga gca acc tta att aat gcc aca 672		
Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr		
210	215	220
tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc 720		
Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala		
225	230	235 240
aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa 768		
Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys		
245	250	255
cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca 816		
Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser		
260	265	270
cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac 864		
His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr		
275	280	285
aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt 912		
Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe		
290	295	300
caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat 960		
Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn		

305

310

315

320

gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata
1008

Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile

325

330

335

gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act
1056

Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr

340

345

350

cct aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc
1104

Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys

355

360

365

cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc
1152

Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile

370

375

380

tgg tac ctt gct gga ata gcg agc tcg gga gat gaa tgt gcg aaa ccc
1200

Trp Tyr Leu Ala Gly Ile Ala Ser Ser Gly Asp Glu Cys Ala Lys Pro

385

390

395

400

aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att
1248

Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile

405

410

415

act tca aaa act ggt atc taa
1269

Thr Ser Lys Thr Gly Ile

420

<210> 4
 <211> 422
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
 1 5 10 15

Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala
 20 25 30

Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
 35 40 45

Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
 50 55 60

Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
 65 70 75 80

Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
 85 90 95

Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
 100 105 110

Gly Val Leu Ala His Met Leu Leu Ile Ser Arg Phe His Ser Thr Glu
 115 120 125

Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
 130 135 140

Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
 145 150 155 160

Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
 165 170 175

Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
 180 185 190

Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
 195 200 205

Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 210 215 220

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
 225 230 235 240

Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
 245 250 255

Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
 260 265 270

His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
 275 280 285

Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
 290 295 300

Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
 305 310 315 320

Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
 325 330 335

Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
340 345 350

Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
355 360 365

Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
370 375 380

Trp Tyr Leu Ala Gly Ile Ala Ser Ser Gly Asp Glu Cys Ala Lys Pro
385 390 395 400

Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
405 410 415

Thr Ser Lys Thr Gly Ile
420

<210> 5
<211> 28
<212> DNA
<213> synthetic construct

<400> 5
tgcacatcaagc aaacagttta ttgagatc
28

<210> 6
<211> 25
<212> DNA
<213> synthetic construct

<400> 6
cctgttcct acacaaathc agtac
25

<210> 7
<211> 28
<212> DNA

<213> synthetic construct

<400> 7

tgacttggat gtagacctcg accttcag
28

<210> 8

<211> 22

<212> DNA

<213> synthetic construct

<400> 8

ggaatagtga gctcgggaga tg
22

<210> 9

<211> 28

<212> DNA

<213> synthetic construct

<400> 9

tcactgttca ttatgtgaga tataatca
28

AA:
67x
<210> 10

<211> 27

<212> DNA

<213> synthetic construct

<400> 10

caccattgat tcaagtctct ggctcat
27
